SEQUENCE LISTING

<110> University of Utah Research Foundation
Yale University
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Splawski, Igor
Keating, Mark T
Goldstein, Steve A.N.

<120> MinK-Related Genes, Formation of Potassium Channels and Association with Cardiac Arrythmia

<130> 2323-150.a

<140> 09/550,163
<141> 2000-04-14

<150> US 60/129,404
<151> 1999-04-15

<160> 22
<170> PatentIn version 3.1/2.0

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Met Ser Thr Leu Ser Asn Phe Thr Gln Thr Leu Glu
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gac gtc ttc cga agg att ttt att act tat atg gac aat tgg cgc cag 157
Asp Val Phe Arg Arg Ile Phe Ile Thr Tyr Met Asp Asn Trp Arg Gln
15 20 25

aac aca aca gct gag caa gag gcc ctc caa gcc aaa gtt gat gct gag 205
Asn Thr Thr Ala Glu Gln Glu Ala Leu Gln Ala Lys Val Asp Ala Glu
30 35 40

aac ttc tac tat gtc atc ctg tac ctc atg gtg atg att gga atg ttc 253
Asn Phe Tyr Tyr Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe
45 50 55 60

tct ttc atc atc gtg gcc atc ctg gtg agc act gtg aaa tcc aag aga 301
Ser Phe Ile Ile Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg
65 70 75

cgg gaa cac tcc aat gac ccc tac cac cag tac att gta gag gac tgg 349
Arg Glu His Ser Asn Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp
80 85 90

cag gaa aag tac aag agc caa atc ttg aat cta gaa gaa tcg aag gcc 397
Gln Glu Lys Tyr Lys Ser Gln Ile Leu Asn Leu Glu Glu Ser Lys Ala
95 100 105

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acc atc cat gag aac att ggt gcg gct ggg ttc aaa atg tcc ccc       442
Thr Ile His Glu Asn Ile Gly Ala Ala Gly Phe Lys Met Ser Pro
   110                 115                 120

tgataaggga gaaaggcacc aagctaacat ctgacgtcca gacatgaaga gatgccagtg 502

ccacgaggca aatccaaatt gtctttgctt agaagaaagt gagttccttg ctctttgttg 562

agaattttca tggagattat gtggttggcc aataaagata gatgacattt caatctcagt 622

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<213> Homo sapiens

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             20                  25                  30

Glu Gln Glu Ala Leu Gln Ala Lys Val Asp Ala Glu Asn Phe Tyr Tyr
         35                  40                  45

Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe Ser Phe Ile Ile
     50                  55                  60

Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg Arg Glu His Ser
 65                  70                  75                  80

Asn Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp Gln Glu Lys Tyr
                 85                  90                  95

Lys Ser Gln Ile Leu Asn Leu Glu Glu Ser Lys Ala Thr Ile His Glu
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Asn Ile Gly Ala Ala Gly Phe Lys Met Ser Pro
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Thr Gln Thr Leu Glu Asp Ala Phe Lys Lys Val Phe Ile Thr Tyr Met
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gac agc tgg agg agg aac aca aca gcc gaa caa cag gcg ctc cag gcc   151
Asp Ser Trp Arg Arg Asn Thr Thr Ala Glu Gln Gln Ala Leu Gln Ala
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aga gtg gat gcc gag aac ttc tac tac gtc atc ctg tac ctc atg gtg   199
Arg Val Asp Ala Glu Asn Phe Tyr Tyr Val Ile Leu Tyr Leu Met Val
 40                  45                  50                  55

atg atc ggc atg ttc gcc ttc atc gtg gtg gcc atc ctg gtg agc acg   247
Met Ile Gly Met Phe Ala Phe Ile Val Val Ala Ile Leu Val Ser Thr
                 60                  65                  70

gtg aag tcg aag cgg cgg gag cac tcc cag gac ccg tac cac cag tac   295
Val Lys Ser Lys Arg Arg Glu His Ser Gln Asp Pro Tyr His Gln Tyr
             75                  80                  85

atc gtg gag gat tgg cag cag aag tat agg agt cag atc ttg cat ctg   343
Ile Val Glu Asp Trp Gln Gln Lys Tyr Arg Ser Gln Ile Leu His Leu
         90                  95                 100

gaa gac tcc aag gcc acc atc cat gag aac ctg ggg gcg acg ggg ttc   391
Glu Asp Ser Lys Ala Thr Ile His Glu Asn Leu Gly Ala Thr Gly Phe
    105                 110                 115

aca gtg tca ccc tgataaagaa cgagagtcca tctgcccagg aaggggtgct       443
Thr Val Ser Pro
120

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             20                  25                  30

Glu Gln Gln Ala Leu Gln Ala Arg Val Asp Ala Glu Asn Phe Tyr Tyr
         35                  40                  45

Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe Ala Phe Ile Val
     50                  55                  60

Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg Arg Glu His Ser
 65                  70                  75                  80

Gln Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp Gln Gln Lys Tyr
                 85                  90                  95

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Asn Leu Gly Ala Thr Gly Phe Thr Val Ser Pro
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Met Glu Thr Thr Asn Gly Thr
1 5

gag acc tgg tat gag agc ctg cat gcc gtg ctg aag gct cta aat gcc 161
Glu Thr Trp Tyr Glu Ser Leu His Ala Val Leu Lys Ala Leu Asn Ala
10 15 20

act ctt cac agc aat ttg ctc tgc cgg cca ggg cca ggg ctg ggg cca 209
Thr Leu His Ser Asn Leu Leu Cys Arg Pro Gly Pro Gly Leu Gly Pro
25 30 35

gac aac cag act gaa gag agg cgg gcc agc cta cct ggc cgt gat gac 257
Asp Asn Gln Thr Glu Glu Arg Arg Ala Ser Leu Pro Gly Arg Asp Asp
40 45 50 55

aac tcc tac atg tac att ctc ttt gtc atg ttt cta ttt gct gta act 305
Asn Ser Tyr Met Tyr Ile Leu Phe Val Met Phe Leu Phe Ala Val Thr
60 65 70

gtg ggc agc ctc atc ctg gga tac acc cgc tcc cgc aaa gtg gac aag 353
Val Gly Ser Leu Ile Leu Gly Tyr Thr Arg Ser Arg Lys Val Asp Lys
75 80 85

cgt agt gac ccc tat cat gtg tat atc aag aac cgt gtg tct atg atc 401
Arg Ser Asp Pro Tyr His Val Tyr Ile Lys Asn Arg Val Ser Met Ile
90 95 100

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ccagaactct gctgtggact gcatcaggtc t 492

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35 40 45

Ser Leu Pro Gly Arg Asp Asp Asn Ser Tyr Met Tyr Ile Leu Phe Val
50 55 60

Met Phe Leu Phe Ala Val Thr Val Gly Ser Leu Ile Leu Gly Tyr Thr
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aaggaactga ggggttgtgg gacatccacg aagagatcct caaagatgtc tcagagccag 180

cagagtctct gaactgtttg atcacattcc agctcttccc atacctcaat atctgttgct 240

atg gag act tcc aac ggg act gag acc tgg tac atg agc ctc cat gct 288
Met Glu Thr Ser Asn Gly Thr Glu Thr Trp Tyr Met Ser Leu His Ala
1 5 10 15

gtg ctg aag gct ctg aac aca acc ctt cac agt cac ttg ctc tgc cgg 336
Val Leu Lys Ala Leu Asn Thr Thr Leu His Ser His Leu Leu Cys Arg
20 25 30

cct ggg cca gga cca ggg cca gac aat caa act gag gat cgt cgg gct 384
Pro Gly Pro Gly Pro Gly Pro Asp Asn Gln Thr Glu Asp Arg Arg Ala
35 40 45

agc ctt cct ggt cgt aat gac aac tcc tac atg tat att ctc ttt gtc 432
Ser Leu Pro Gly Arg Asn Asp Asn Ser Tyr Met Tyr Ile Leu Phe Val
50 55 60

atg ttc cta ttt gcc gtc act gtg ggc agt ctc atc ctg gga tat acc 480
Met Phe Leu Phe Ala Val Thr Val Gly Ser Leu Ile Leu Gly Tyr Thr
65 70 75 80

cgt tca cgc aaa gtg gac aaa cgt agt gac ccc tat cat gtg tac atc 528
Arg Ser Arg Lys Val Asp Lys Arg Ser Asp Pro Tyr His Val Tyr Ile
85 90 95

aag aac cgt gtg tct atg atc tgatgtgagg aacctgaaga caatggaaga 579
Lys Asn Arg Val Ser Met Ile
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cagagaagag ggactgatag gcccagtctt gtggatgaga catttttcga gacacagatg 759

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gaagaggaag ctgtggcgaa gggaaatggg gcagaaagat gctctggata tataatcttt 879

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			20					25					30		
Pro	Gly	Pro	Gly	Pro	Gly	Pro	Asp	Asn	Gln	Thr	Glu	Asp	Arg	Arg	Ala
		35					40					45			
Ser	Leu	Pro	Gly	Arg	Asn	Asp	Asn	Ser	Tyr	Met	Tyr	Ile	Leu	Phe	Val
	50					55					60				
Met	Phe	Leu	Phe	Ala	Val	Thr	Val	Gly	Ser	Leu	Ile	Leu	Gly	Tyr	Thr
65					70					75					80
Arg	Ser	Arg	Lys	Val	Asp	Lys	Arg	Ser	Asp	Pro	Tyr	His	Val	Tyr	Ile
				85					90					95	
Lys	Asn	Arg	Val	Ser	Met	Ile									
			100												

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ttaatagatg aatttttttc ctttattttc ttcctgcttt tctttgttct aaggaaacat 180

tgttttgaat ttaaaatagt ttggttttgg aaacacaatg taaactttgt ttctgctcag 240

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tca atg ctg aaa atg gag cct ctg aac agc acg cac ccc ggc acc gcc   648
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     1               5                  10                  15

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Ala Ser Ser Ser Pro Leu Glu Ser Arg Ala Ala Gly Gly Gly Ser Gly
                20                  25                  30

aat ggc aac gag tac ttc tac att ctg gtt gtc atg tcc ttc tac ggc   744
Asn Gly Asn Glu Tyr Phe Tyr Ile Leu Val Val Met Ser Phe Tyr Gly
            35                  40                  45

att ttc ttg atc gga atc atg ctg ggc tac atg aaa tcc aag agg cgg   792
Ile Phe Leu Ile Gly Ile Met Leu Gly Tyr Met Lys Ser Lys Arg Arg
        50                  55                  60

gag aag aag tcc agc ctc ctg ctg ctg tac aaa gac gag gag cgg ctc   840
Glu Lys Lys Ser Ser Leu Leu Leu Leu Tyr Lys Asp Glu Glu Arg Leu
    65                  70                  75

tgg ggg gag gcc atg aag ccg ctg ccc gtg gtg tcg ggc ctg agg tcg   888
Trp Gly Glu Ala Met Lys Pro Leu Pro Val Val Ser Gly Leu Arg Ser
80                  85                  90                  95

gtg cag gtg ccc ctg atg ctg aac atg ctg cag gag agc gtg gcg ccc   936
Val Gln Val Pro Leu Met Leu Asn Met Leu Gln Glu Ser Val Ala Pro
                100                 105                 110

gcg ctg tcc tgc acc ctc tgt tcc atg gaa ggg gac agc gtg agc tcc   984
Ala Leu Ser Cys Thr Leu Cys Ser Met Glu Gly Asp Ser Val Ser Ser
            115                 120                 125

gag tcc tcc tcc ccg gac gtg cac ctc acc att cag gag gag ggg gca   1032
Glu Ser Ser Ser Pro Asp Val His Leu Thr Ile Gln Glu Glu Gly Ala
        130                 135                 140

gac gat gag ctg gag gag acc tcg gag acg ccc ctc aac gag agc agc   1080
Asp Asp Glu Leu Glu Glu Thr Ser Glu Thr Pro Leu Asn Glu Ser Ser
    145                 150                 155

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Glu Gly Ser Ser Glu Asn Ile His Gln Asn Ser
160                 165                 170

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             20                  25                  30

Gly Asn Glu Tyr Phe Tyr Ile Leu Val Val Met Ser Phe Tyr Gly Ile
         35                  40                  45

Phe Leu Ile Gly Ile Met Leu Gly Tyr Met Lys Ser Lys Arg Arg Glu
     50                  55                  60

Lys Lys Ser Ser Leu Leu Leu Leu Tyr Lys Asp Glu Glu Arg Leu Trp
 65                  70                  75                  80

Gly Glu Ala Met Lys Pro Leu Pro Val Val Ser Gly Leu Arg Ser Val
                 85                  90                  95

Gln Val Pro Leu Met Leu Asn Met Leu Gln Glu Ser Val Ala Pro Ala
            100                 105                 110

Leu Ser Cys Thr Leu Cys Ser Met Glu Gly Asp Ser Val Ser Ser Glu
        115                 120                 125

Ser Ser Ser Pro Asp Val His Leu Thr Ile Gln Glu Glu Gly Ala Asp
    130                 135                 140

Asp Glu Leu Glu Glu Thr Ser Glu Thr Pro Leu Asn Glu Ser Ser Glu
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Gly Ser Ser Glu Asn Ile His Gln Asn Ser
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Met Leu Arg Met Glu Pro Leu Asn Ser
1   5

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aca tac ccc agc gct gca gcc tcc agc agc ccc ctc gag tcc cat gtg   160
Thr Tyr Pro Ser Ala Ala Ala Ser Ser Ser Pro Leu Glu Ser His Val
 10                  15                  20                  25

cct agt aac agc agt ggt aat ggc aat gaa tac ttc tat att ttg gtc   208
Pro Ser Asn Ser Ser Gly Asn Gly Asn Glu Tyr Phe Tyr Ile Leu Val
                 30                  35                  40

gtt atg tcc ttc tat ggc gtt ttc ctg atc gga atc atg ctg ggc tac   256
Val Met Ser Phe Tyr Gly Val Phe Leu Ile Gly Ile Met Leu Gly Tyr
             45                  50                  55

atg aaa tcc aag agg cgg gag aag aag tcc agc ctt ctg ctg ttg tac   304
Met Lys Ser Lys Arg Arg Glu Lys Lys Ser Ser Leu Leu Leu Leu Tyr
         60                  65                  70

aaa gac gag gag agg ctg tgg ggg gag gct atg aag ccg cta cct atg   352
Lys Asp Glu Glu Arg Leu Trp Gly Glu Ala Met Lys Pro Leu Pro Met
     75                  80                  85

atg tcc ggc ttg agg tca ggg cag gtg ccc atg atg ctg aat atg ctg   400
Met Ser Gly Leu Arg Ser Gly Gln Val Pro Met Met Leu Asn Met Leu
 90                  95                 100                 105

cag gag agt gtg gcg ccg gca ctg tcc tgc act ctt tgc tcg atg gaa   448
Gln Glu Ser Val Ala Pro Ala Leu Ser Cys Thr Leu Cys Ser Met Glu
                110                 115                 120

ggg gac agt gtg agc tcc gag tcc tcc tct cct gat gtg cac ctt ccc   496
Gly Asp Ser Val Ser Ser Glu Ser Ser Ser Pro Asp Val His Leu Pro
            125                 130                 135

atc cag gag gag ggg gct gat gac gag ctg gag gag acc tcc gag acg   544
Ile Gln Glu Glu Gly Ala Asp Asp Glu Leu Glu Glu Thr Ser Glu Thr
        140                 145                 150

cct ctc aac gac agc agt gaa ggc tct tcc gag aac atc cac cag aat   592
Pro Leu Asn Asp Ser Ser Glu Gly Ser Ser Glu Asn Ile His Gln Asn
    155                 160                 165

tcc tagcacccac caggtgctag gaggtagctc cgtaagctac acttgacaga        645
Ser
170

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gggggccgtt taagttgaaa gaagccaagt taagtttggc ctcgtgcctg gaatcacttg 2265

aattctgaaa ctttactgcg acagacatgt gcgttgtcac attttccatt gcttaatcct 2325

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<212> PRT
<213> Mus musculus

<400> 12

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35 40 45

Phe Leu Ile Gly Ile Met Leu Gly Tyr Met Lys Ser Lys Arg Arg Glu
50 55 60

Lys Lys Ser Ser Leu Leu Leu Leu Tyr Lys Asp Glu Glu Arg Leu Trp
65 70 75 80

Gly Glu Ala Met Lys Pro Leu Pro Met Met Ser Gly Leu Arg Ser Gly
85 90 95

Gln Val Pro Met Met Leu Asn Met Leu Gln Glu Ser Val Ala Pro Ala
100 105 110

Leu Ser Cys Thr Leu Cys Ser Met Glu Gly Asp Ser Val Ser Ser Glu
115 120 125

Ser Ser Ser Pro Asp Val His Leu Pro Ile Gln Glu Glu Gly Ala Asp
130 135 140

Asp Glu Leu Glu Glu Thr Ser Glu Thr Pro Leu Asn Asp Ser Ser Glu
145 150 155 160

Gly Ser Ser Glu Asn Ile His Gln Asn Ser
165 170

<210> 13
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer for mutation screening

<400> 13
ccgttttcct aaccttgttc g 21

<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer for mutation screening

<400> 14
agcatcaact ttggcttgga g 21

<210> 15
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer for mutation screening

<400> 15
gtcttccgaa ggatttttat tac 23

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence
<220>

<223> Description of Artificial Sequence:PCR primer for mutation screening

<400> 16
gttcccgtct cttggatttc a 21

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer for mutation screening

<400> 17
aatgttctct ttcatcatcg tg 22

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer for mutation screening

<400> 18
tgtctggacg tcagatgtta g 21

<210> 19
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HA residues for epitope mapping

<220>
<221> PEPTIDE
<222> (10)
<223> Xaa represents encoded stop codon.

<400> 19
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Xaa
1 5 10

<210> 20
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:cmyc residues for epitope-mapping

<220>
<221> PEPTIDE
<222> (15)

<223> Xaa represents encoded stop codon.

<400> 20
Ile Ser Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Xaa
1 5 10 15

<210> 21
<211> 130
<212> PRT
<213> rattus norvgecicus

<400> 3

Met Ala Leu Ser Asn Ser Thr Thr Val Leu Pro Phe Leu Ala Ser Leu
1 5 10 15

Trp Gln Glu Thr Asp Glu Pro Gly Gly Asn Met Ser Ala Asp Leu Ala
20 25 30

Arg Arg Ser Gln Leu Arg Asp Asp Ser Lys Leu Glu Ala Leu Tyr Ile
35 40 45

Leu Met Val Leu Gly Phe Phe Gly Phe Phe Thr Leu Gly Ile Met Leu
50 55 60

Ser Tyr Ile Arg Ser Lys Lys Leu Glu His Ser His Asp Pro Phe Asn
65 70 75 80

Val Tyr Ile Glu Ser Asp Ala Trp Gln Glu Lys Gly Lys Ala Leu Phe
85 90 95

Gln Ala Arg Val Leu Glu Ser Phe Arg Ala Cys Tyr Val Ile Glu Asn
100 105 110

Gln Ala Ala Val Glu Gln Pro Ala Thr His Leu Pro Glu Leu Lys Pro
115 120 125

Leu Ser
130

<210> 22
<211> 129
<212> PRT
<213> homo sapiens

<400> 4

Met Ile Leu Ser Asn Thr Thr Ala Val Thr Pro Phe Leu Thr Lys Leu
1 5 10 15

Trp Gln Glu Thr Val Gln Gln Gly Gly Asn Met Ser Gly Leu Ala Arg
20 25 30

Arg Ser Pro Arg Ser Gly Asp Gly Lys Leu Glu Ala Leu Tyr Val Leu
35 40 45

Met Val Leu Gly Phe Phe Gly Phe Phe Thr Leu Gly Ile Met Leu Ser
50 55 60

Tyr Ile Arg Ser Lys Lys Leu Glu His Ser Asn Asp Pro Phe Asn Val
65 70 75 80

Tyr Ile Glu Ser Asp Ala Trp Gln Glu Lys Asp Lys Ala Tyr Val Gln
85 90 95

Ala Arg Val Leu Glu Ser Tyr Arg Ser Cys Tyr Val Val Glu Asn His
100 105 110

Leu Ala Ile Glu Gln Pro Asn Thr His Leu Pro Glu Thr Lys Pro Ser
115 120 125

Pro